

Figure 1

1  
ATGGCTCCCTTAGCCGAAGTCGGGGGCTTTCTGGGCGGCCTGGAG  
MetAlaProLeuAlaGluValGlyGlyPheLeuGlyGlyLeuGlu  
46  
GGCTTGGGCCAGCAGGTGGGTTCGCATTTCTGTGCCTCCTGCC  
GlyLeuGlyGlnGlnValGlySerHisPheLeuLeuProProAla  
91  
GGGGAGCGGCCCGCTGCTGGGCGAGCGCAGGAGCGCGCGGAG  
GlyGluArgProProLeuLeuGlyGluArgArgSerAlaAlaGlu  
136  
CGGAGCGCGCGCGGGCGGGGCTGCGCAGCTGGCGCACCTG  
ArgSerAlaArgGlyGlyProGlyAlaAlaGlnLeuAlaHisLeu  
181  
CACGGCATCCTGCGCCCGGCAGCTCTATTGCCGCACCGCTTC  
HisGlyIleLeuArgArgArgGlnLeuTyrCysArgThrGlyPhe  
226  
CACCTGCAGATCCTGCCCCACGGCAGCGTGACGGGCACCCGGCAG  
HisLeuGlnIleLeuProAspGlySerValGlnGlyThrArgGln  
271  
GACCACAGCCTCTTCGGTATCTTGAATTCATCAGTGTGGCAGTG  
AspHisSerLeuPheGlyIleLeuGluPheIleSerValAlaVal  
316  
GGACTGGTCAGTATTAGAGGTGTGGACAGTGGTCTCTATCTTGA  
GlyLeuValSerIleArgGlyValAspSerGlyLeuTyrLeuGly  
361  
ATGAATGACAAAGGAGAACTCTATGGATCAGAGAACTTACTTCC  
MetAsnAspLysGlyGluLeuTyrGlySerGluLysLeuThrSer  
406  
GAATGCATCTTTAGGGAGCAGTTTGAAGAGAACTGGTATAACACC  
GluCysIlePheArgGluGlnPheGluGluAsnTrpTyrAsnThr  
451  
TATTCATCTAACATATATAAACATGGAGACACTGGCCGCAGGTAT  
TyrSerSerAsnIleTyrLysHisGlyAspThrGlyArgArgTyr  
496  
TTTGTGGCACTTAACAAAGACGGAACCTCAAGAGATGGCGCCAGG  
PheValAlaLeuAsnLysAspGlyThrProArgAspGlyAlaArg  
541  
TCCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTG  
SerLysArgHisGlnLysPheThrHisPheLeuProArgProVal  
586  
GATCCAGAAAGAGTTCCAGAATTGTACAAGGACCTACTGATGTAC  
AspProGluArgValProGluLeuTyrLysAspLeuLeuMetTyr  
631  
ACT  
Thr

```

Query:      170 TGGCGCACCTGCACGGCATCTCTGCGCCGCCGGCAGCTCTATTGCCGCACCGGCTTCCACC 229
            ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:       2 TGGATCATTTAAAGGGGATTCTCAGGCGGAGGCAGCTATACTGCAGGACTGGATTTCACT 61

Query:     230 TGCAGATCCTGCCCCACGGCAGCGTGCAGGGCACCCGGCAGGACCACAGCCTCTTCGGTA 289
            | ||| ||| ||| ||| ||| | |||| ||| ||| ||| ||| ||| ||| |||
Sbjct:     62 TAGAAATCTTCCCCAATGGTACTATCCAGGGAACCAGGAAAGACCACAGCCGATTTGGCA 121

Query:     290 TCTTGAATTTCATCAGTGTGGCAGTGGGACTGGTCAGTATTAGAGGTGTGGACAGTGGTC 349
            | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:    122 TTCTGGAATTTATCAGTATAGCAGTGGGCCTGGTCAGCATTTCGAGGCGTGGACAGTGGAC 181

Query:     350 TCTATCTTGGAATGAATGACAAAGGAGAACTCTATGGATCAGAGAACTTACTTCCGAAT 409
            |||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:    182 TCTACCTCGGGATGAATGAGAAGGGGGAGCTGTATGGATCAGAAAACTAACCCAAGAGT 241

Query:     410 GCATCTTTAGGGAGCAGTTTGAAGAGAACTGGTATAACACCTATTCATCTAACATATATA 469
            | | | ||| ||| |||| |||| |||| |||| |||| ||| ||| ||| ||||
Sbjct:    242 GTGTATTAGAGAACAGTTTGAAGAAAACCTGGTATAATACGTACTCGTCAAACCTATATA 301

Query:     470 AACATGGAGACACTGGCCGCAGGTATTTTGTGGCACTTAACAAAGACGGAACCTCAAGAG 529
            | || | |||| |||| |||| |||| |||| |||| ||| ||| ||| ||||
Sbjct:    302 AGCAGTGGACACTGGAAGGCGATACTATGTTGCATTAAATAAAGATGGGACCCCGAGAG 361

Query:     530 ATGGCGCCAGGTCCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTGGATC 589
            || | ||| ||| ||| |||| |||| |||| |||| |||| |||| |||| |||
Sbjct:    362 AAGGGACTAGGACTAAACGGCACCAGAAATTCACACATTTTTTACCTAGACCAGTGGACC 421

Query:     590 CAGA 593
            |||
Sbjct:    422 CCGA 425

```

### Figure 3

>gb:GenBank accession number -ID:AB020858|acc:AB020858 Homo sapiens genomic DNA of p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 1/11 - Homo sapiens, 100000 bp.

Minus Strand HSPs:

#### A.

Score = 1430 (214.6 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126  
Identities = 288/289 (99%), Positives = 288/289 (99%), Strand = Minus / Plus

```
Query:   289 TACCGAAGAGGCTGTGGTCTCGCGGGTGCCCTGCACGCTGCCGTCGGGCAGGATCTGCA 230
          |||
Sbjct: 15927 TACCGAAGAGGCTGTGGTCTCGCGGGTGCCCTGCACGCTGCCGTCGGGCAGGATCTGCA 15986

Query:   229 GGTGGAAGCCGGTGCGGCAATAGAGCTGCCGGCGCGCAGGATGCCGTGCAGGTGCGCCA 170
          |||
Sbjct: 15987 GGTGGAAGCCGGTGCGGCAATAGAGCTGCCGGCG-CG-CAGGATGCCGTGCAGGTGCGCCA 16045

Query:   169 GCTGCGCAGCCCCCGGCCCGCCGCGCGCTCCGCTCCGCCGCGCTCCTGCGCTCGCCCA 110
          |||
Sbjct: 16046 GCTGCGCAGCCCCCGGCCCGCCGCGCGCTCCGCTCCGCCGCGCTCCTGCGCTCGCCCA 16105

Query:   109 GCAGCGGCGCGCTCCCCGGCAGGAGGCAACAGGAAATGCGAACCCACCTGCTGGCCCA 50
          |||
Sbjct: 16106 GCAGCGGCGCGCTCCCCGGCAGGAGGCAACAGGAAATGCGAACCCACCTGCTGGCCCA 16165

Query:    49 AGCCCTCCAGGCCGCCAGAAAGCCCCCGACTTCGGCTAAGGGAGCCAT 1
          |||
Sbjct: 16166 AGCCCTCCAGGCCGCCAGAAAGCCCCCGACTTCGGCTAAGGGAGCCAT 16214
```

#### B.

Score = 1224 (183.6 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126  
Identities = 250/255 (98%), Positives = 250/255 (98%), Strand = Minus / Plus

```
Query:   633 AGTGATACATCAGTAGGTCCTTGTACAATTCTGGAACCTTTCTGGATCCACTGGTCTAGG 574
          |||
Sbjct: 7257 AGTGATACATCAGTAGGTCCTTGTACAATTCTGGAACCTTTCTGGATCCACTGGTCTAGG 7316

Query:   573 TAAGAAATGTGTAAATTTCTGATGCCTCTTGACCTGGCGCCATCTCTTGAGTTCCGTC 514
          |||
Sbjct: 7317 TAAGAAATGTGTAAATTTCTGATGCCTCTTGACCTGGCGCCATCTCTTGAGTTCCGTC 7376

Query:   513 TTTGTTAAGTGCCACAAAATACCTGCGGCCAGTGTCTCCATGTTTATATATGTTAGATGA 454
          |||
Sbjct: 7377 TTTGTTAAGTGCCACAAAATACCTGCGGCCAGTGTCTCCATGTTTATATATGTTAGATGA 7436

Query:   453 ATAGGTGTTATACCAGTTCTCTTCAAACCTGCTCCCTAAAGATGCATTGGAAGTAAGTTT 394
          |||
Sbjct: 7437 ATAGGTGTTATACCAGTTCTCTTCAAACCTGCTCCCTAAAGATGCATTGGAAGTAAGTTT 7496

Query:   393 CTC-TGATCCATAGA 380
          |||
Sbjct: 7497 CTCCTGAAAGAGAGA 7511
```

## Figure 3 (cont.)

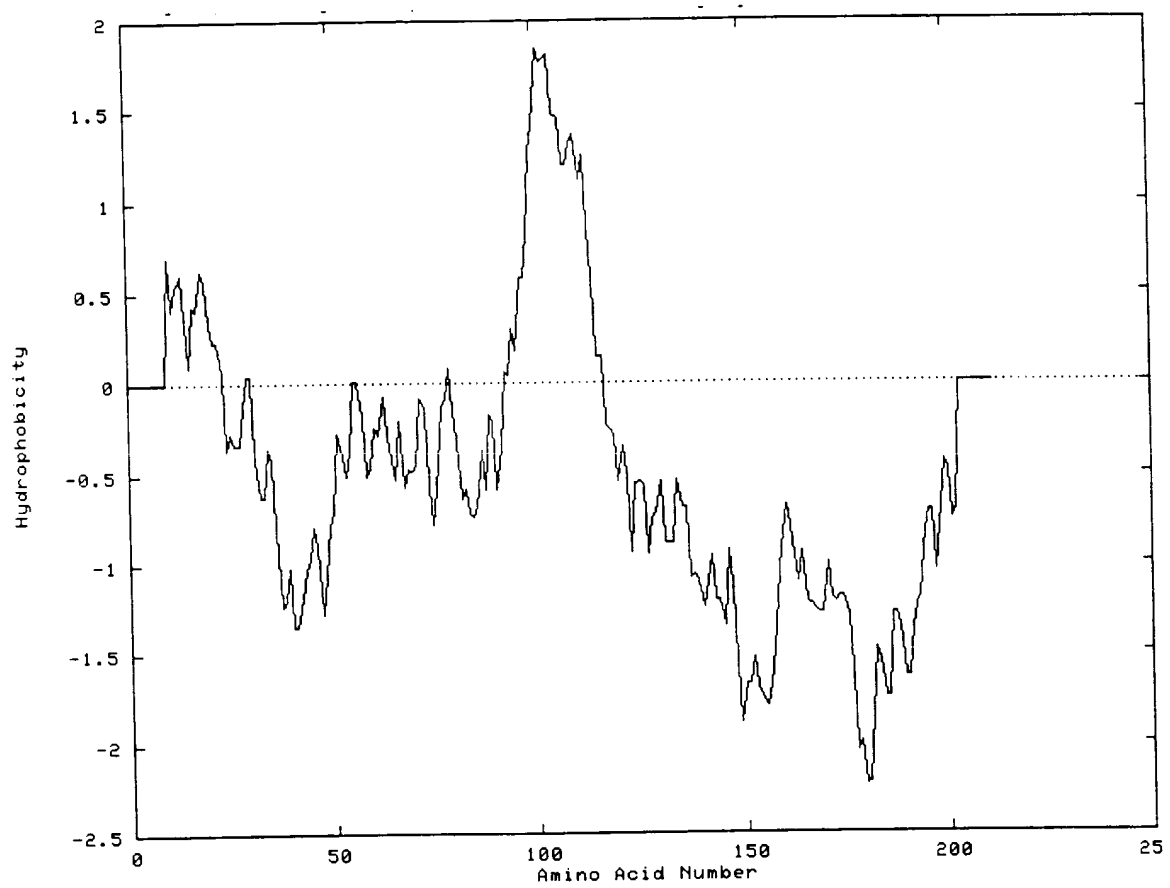
### C.

Score = 530 (79.5 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126  
Identities = 106/106 (100%), Positives = 106/106 (100%), Strand = Minus / Plus

```
Query:   391 CTGATCCATAGAGTTCTCCTTTGTCATTTCATTCCTCAAGATAGAGACCACTGTCCACACCTC 332
          |||
Sbjct:  9837 CTGATCCATAGAGTTCTCCTTTGTCATTTCATTCCTCAAGATAGAGACCACTGTCCACACCTC 9896

Query:   331 TAATACTGACCAGTCCCCTGCCCACACTGATGAATTCCAAGATACC 286
          |||
Sbjct:  9897 TAATACTGACCAGTCCCCTGCCCACACTGATGAATTCCAAGATACC 9942
```

Figure 4



## Figure 5

ptnr:SWISSPROT-ACC:P31371 GLIA-ACTIVATING FACTOR PRECURSOR (GAF) (FIBROBLAST GROWTH FACTOR-9) (FGF-9) (HBGF-9) - HOMO SAPIENS (HUMAN), 208 aa. Identities = 147/208 (70%), Positives = 170/208 (81%)

```
Query:      1 MAPLAEVGGFLGGLEGLGQQVGSHFLPPAGERPPLLGERRSAAERSARG-GPGAAQLAH 59
            |||| ||| + | + + | + +|| + ||| + +| || |||
Sbjct:      1 MAPLGEVGNVFGVQDAV--PFGNVPVLPV--DSPVLLSDHLGQSEAGGLPRGPAVTDLDH 56

Query:     60 LHGILRRRQLYCRTGFHLQILPDGSVQGTQRQDHSLSFGILEFISVAVGLVSIRGVDSGLYL 119
            | ||||| ||||| ||||| +| | +| +| ||||| +| ||||| ||||| |||||
Sbjct:     57 LKGILRRRQLYCRTGFHLEIFPNGTIQGTQRKDHSRFGILEFISIAVGLVSIRGVDSGLYL 116

Query:    120 GMNDKGELYGSEKLTSECFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA 179
            ||| + ||||| ||||| ||| + ||||| ||||| ||||| + ||| ||||| + ||||| |||||
Sbjct:    117 GMNEKGELYGSEKLTQECVFEENWYNTYSSNLYKHVDTGRRYYVALNKDGTREGT 176

Query:    180 RSKRHQKFTHFLPRPVDPERVPELYKDIL 208
            | + ||||| ||||| ||||| ||||| + ||||| ||||| + ||||| |||||
Sbjct:    177 RTRRHQKFTHFLPRPVDPKVPELYKDIL 205
```

## Figure 6

Length = 208

Plus Strand HSPs:

Score = 775 (272.8 bits), Expect = 3.4e-76, P = 3.4e-76

Identities = 147/208 (70%), Positives = 170/208 (81%), Frame = +1

```
Query:      1 MAPLAEVGGFLGGLEGLGQQVGSFLLPPAGERPPLLGERRSAAERSARG-GPGAAQLAH 59
            |||| ||| + | + + | + +|| + | || + +| || ||
Sbjct:      1 MAPLGEVGSYFGVQDAV--PFGNVPVLPV--DSPVLLNDHLGQSEAGGLPRGPAVTDLDH 56

Query:     60 LHGILRRRQLYCRTGFHLQILPDGSVQGTRQDHSFLGILEFISVAVGLVSIRGVDSGLYL 119
            | ||||| ||||| ||||| +| | +| +| ||| +| ||||| ||||| |||||
Sbjct:     57 LKGILRRRQLYCRTGFHLEIFPNGTIQGTRKDHSRFGILEFISIAVGLVSIRGVDSGLYL 116

Query:    120 GMNDKGELYGSEKLTSECFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA 179
            ||| +| ||||| ||||| || +| ||||| ||||| ||||| +| ||||| ||||| +|
Sbjct:    117 GMNEKGELYGSEKLTQECVFREQFEENWYNTYSSNLYKHVDTGRRYYVALNKDGTREGT 176

Query:    180 RSKRHQKFTHFLPRPVDPERVPELYKDIL 208
            | +| ||||| ||||| ||||| ++| ||||| || +|
Sbjct:    177 RTKRHQKFTHFLPRPVDPAKVPPELYKDIL 205
```

## Figure 7

Length = 208

Plus Strand HSPs:

Score = 775 (272.8 bits), Expect = 3.4e-76, P = 3.4e-76

Identities = 147/208 (70%), Positives = 170/208 (81%), Frame = +1

```
Query:      1 MAPLAEVGGFLGGLEGLGQQVGSFLLPPAGERPPLLGERRSAAERSARG-GPGAAQLAH 59
            |||| ||| + | + + | + +|| + | || + +| || ||
Sbjct:      1 MAPLGEVGSYFGVQDAV--PFGNVPVLPV--DSPVLLSDHLGQSEAGGLPRGPAVTDLDH 56

Query:     60 LHGILRRRQLYCRTGFHLQILPDGSVQGTRQDHSFLFGILEFISVAVGLVSIRGVDSGLYL 119
            | ||||| ||||| ||||| +| | +| +| ||| +| ||||| ||||| |||||
Sbjct:     57 LKGILRRRQLYCRTGFHLEIFPNGTIQGRKDHRSRFGILEFISIAVGLVSIRGVDSGLYL 116

Query:    120 GMNDKGELYGSEKLTSECFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA 179
            ||| +| ||||| ||||| ||| +| ||||| ||||| ||||| +| ||||| |||||
Sbjct:    117 GMNEKGELYGSEKLTQECVFREQFEENWYNTYSSNLYKHVDTGRRYYVALNKDGTREGT 176

Query:    180 RSKRHQKFTHFLPRPVDPERVPELYKDIL 208
            | +| ||||| ||||| ||||| ||| +| ||||| |||||
Sbjct:    177 RTKRHQKFTHFLPRPVDPAKVPPELYKDIL 205
```



## Figure 8

FGF-CX Query Length = 211  
XFGF-20 Sbjct Length = 208

Plus Strand HSPs:

Score = 906 (318.9 bits), Expect = 4.4e-90, P = 4.4e-90  
Identities = 170/211 (80%), Positives = 189/211 (89%), Frame = +1

```
Query:      1 MAPLAEVGGFLGGLEGLGQQVGSFLLPPAGERPPLLGERRSAAERSARGGPGAAQLAHL 60
             |||||+|| |||| + ||| ||||| ||||| + | | + + +|| +| | + |||
Sbjct:      1 MAPLADVGTFLGGYDALGQ-VGSFLLPPAKDSPLLFNDPLAQSERLSRSAP--SDLSHL 57

Query:     61 HGILRRRQLYCRTGFHLQILPDGVSQGTRQDHSFLFGILEFISVAVGLVSIRGVDSGLYLG 120
             ||||| ||||| ||||| ||||| + ||||| ||||| ||||| + ||||| ||||| + |||||
Sbjct:     58 QGILRRRQLYCRTGFHLQILPDGNVQGTRQDHSRFGILEFISVAIGLVSIRGVDTGLYLG 117

Query:    121 MNDKGELYGSEKLTSECIFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGR 180
             ||||| + ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    118 MNDKGELFGSEKLTSECIFREQFEENWYNTYSSNLYKHGDSGRRYFVALNKDGTPRDGTR 177

Query:    181 SKRHQKFTHFLPRPVDPERVPELYKDLLMYT 211
             + ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    178 AKRHQKFTHFLPRPVDPEKVPPELYKDLMGYS 208
```

# FIGURE 9

Sequences analyzed:

1. HUMAN FGF-9 (P31371\_HUMAN FGF-9) [SEQ ID NO:9]
2. MOUSE FGF-9 (P54130\_MOUSE FGF-9) [SEQ ID NO:10]
3. RAT FGF-9 (P36364\_FGF9\_RAT FGF-9) [SEQ ID NO:11]
4. XENOPUS XFGF-20 (BAA83474Xen; Xenopus laevis XFGF-20) [SEQ ID NO:12]
5. FGF-CX (cgAB020858) [SEQ ID NO:2]

Multiple Alignment:

HUMAN FGF-9	M A P L G E V G N Y F G V Q D A V P - - F G N V P V L P - - V D S P V L L S D H L G Q S E A G G L P R G P A V T D L D H
RAT FGF-9	M A P L G E V G S Y F G V Q D A V P - - F G N V P V L P - - V D S P V L L S D H L G Q S E A G G L P R G P A V T D L D H
MOUSE FGF-9	M A P L G E V G S Y F G V Q D A V P - - F G N V P V L P - - V D S P V L L N D H L G Q S E A G G L P R G P A V T D L D H
XENOPUS XFGF-20	M A P L A D V G T F L G G Y D A L G - Q V G S H F L L P P A K D S P L L F N D P L A Q S E R L S R - S A P - - S D L S H
FGF-CX	M A P L A E V G G F L G L E G L G Q Q V G S H F L L P P A G E R P P L L G E R R S A E R S A R - G G P P G A A Q L A H
HUMAN FGF-9	L K G I L R R R R Q L Y C R T G T G F H L E I F P N G T I Q G T R K D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L
RAT FGF-9	L K G I L R R R R Q L Y C R T G T G F H L E I F P N G T I Q G T R K D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L
MOUSE FGF-9	L K G I L R R R R Q L Y C R T G T G F H L E I F P N G T I Q G T R K D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L
XENOPUS XFGF-20	L Q G I L R R R R Q L Y C R T G T G F H L Q I L P D G N V Q G T R Q D H S R F G I L E F I S V A I G L V S I R G V D T G L Y L
FGF-CX	L H G I L R R R R Q L Y C R T G T G F H L Q I L P D G S V Q G T R Q D H S L F G I L E F I S V A V G L V S I R G V D S G L Y L
HUMAN FGF-9	G M N E K G E L Y G S E K L T Q E C V F R E Q F E E N W Y N T Y S S N L Y K H V D T G R R R Y Y V A L N K D G T P R E G T
RAT FGF-9	G M N E K G E L Y G S E K L T Q E C V F R E Q F E E N W Y N T Y S S N L Y K H V D T G R R R Y Y V A L N K D G T P R E G T
MOUSE FGF-9	G M N E K G E L Y G S E K L T Q E C V F R E Q F E E N W Y N T Y S S N L Y K H V D T G R R R Y Y V A L N K D G T P R E G T
XENOPUS XFGF-20	G M N D K G E L F G S E K L T S E C I F R E Q F E E N W Y N T Y S S N L Y K H G D S G R R R Y F V A L N K D G T P R D G T
FGF-CX	G M N D K G E L Y G S E K L T S E C I F R E Q F E E N W Y N T Y S S N I Y K H G D T G R R R Y F V A L N K D G T P R D G A
HUMAN FGF-9	R T K R H Q K F T H F L P R P V D P D K V P E L Y K D I L S Q S
RAT FGF-9	R T K R H Q K F T H F L P R P V D P D K V P E L Y K D I L S Q S
MOUSE FGF-9	R T K R H Q K F T H F L P R P V D P D K V P E L Y K D I L S Q S
XENOPUS XFGF-20	R A K R H Q K F T H F L P R P V D P E K V P E L Y K D L M G Y S
FGF-CX	R S K R H Q K F T H F L P R P V D P E R V P E L Y K D L L M Y T